

FIG. 1

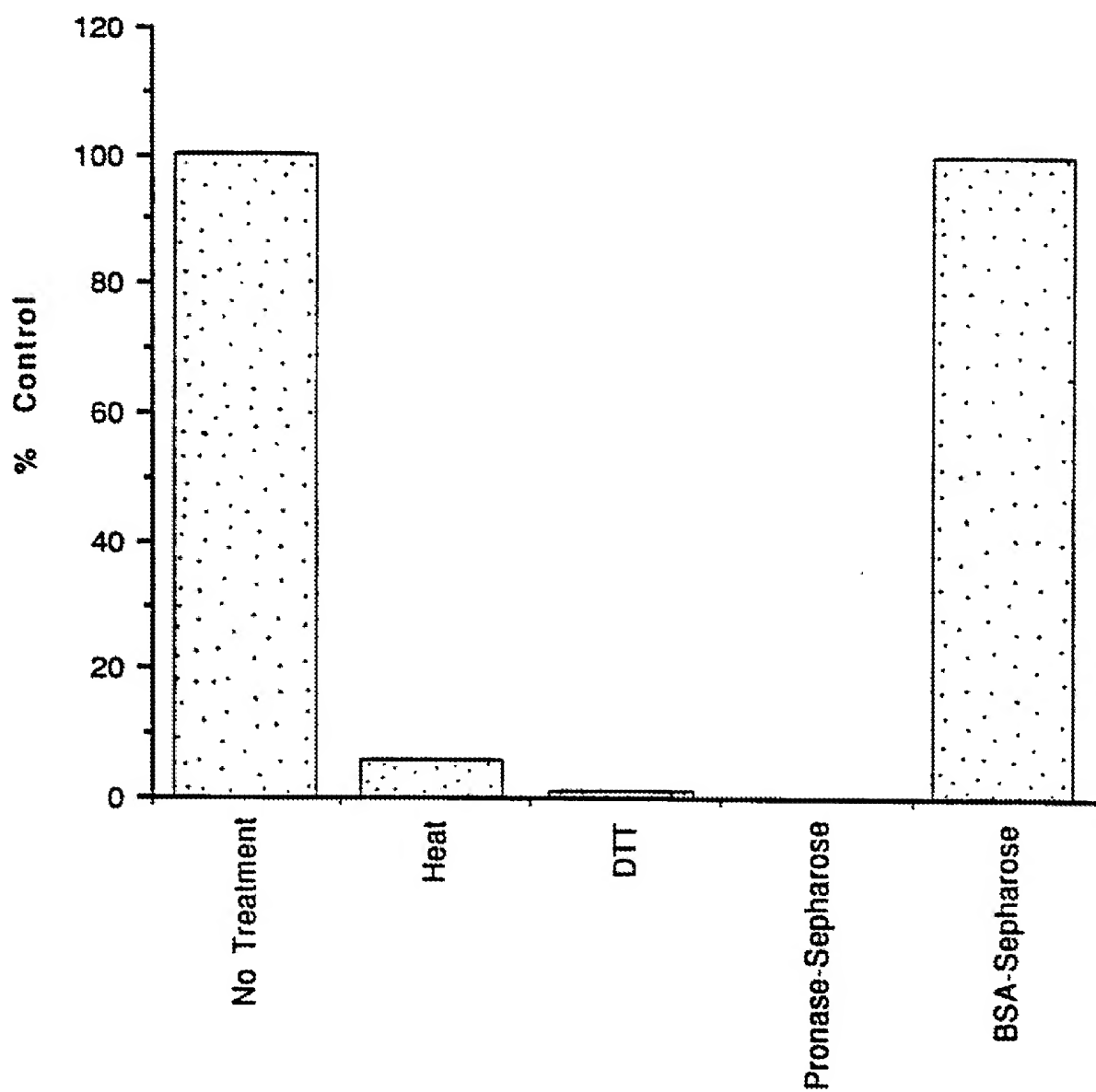


FIG. 2

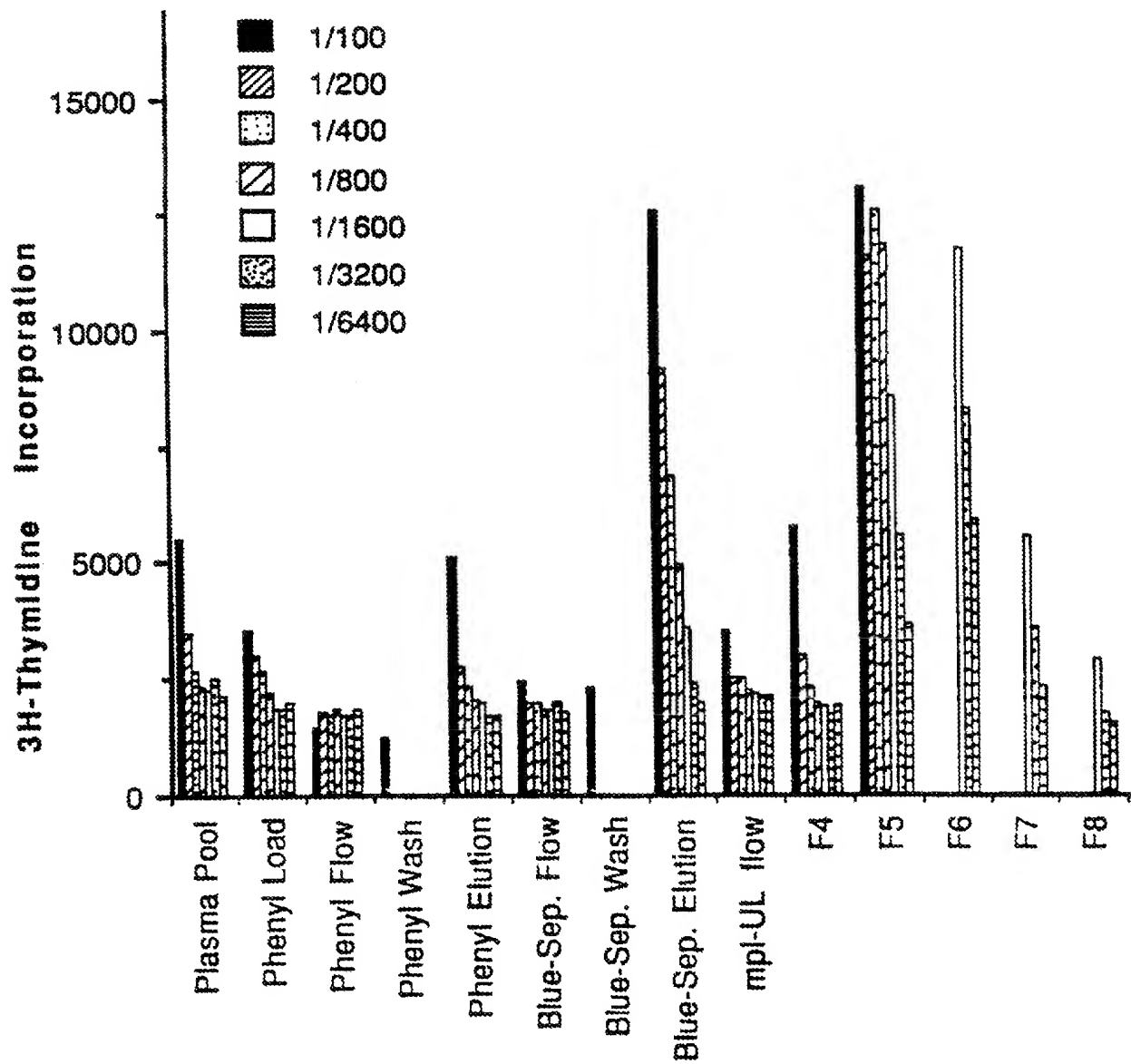


FIG. 3

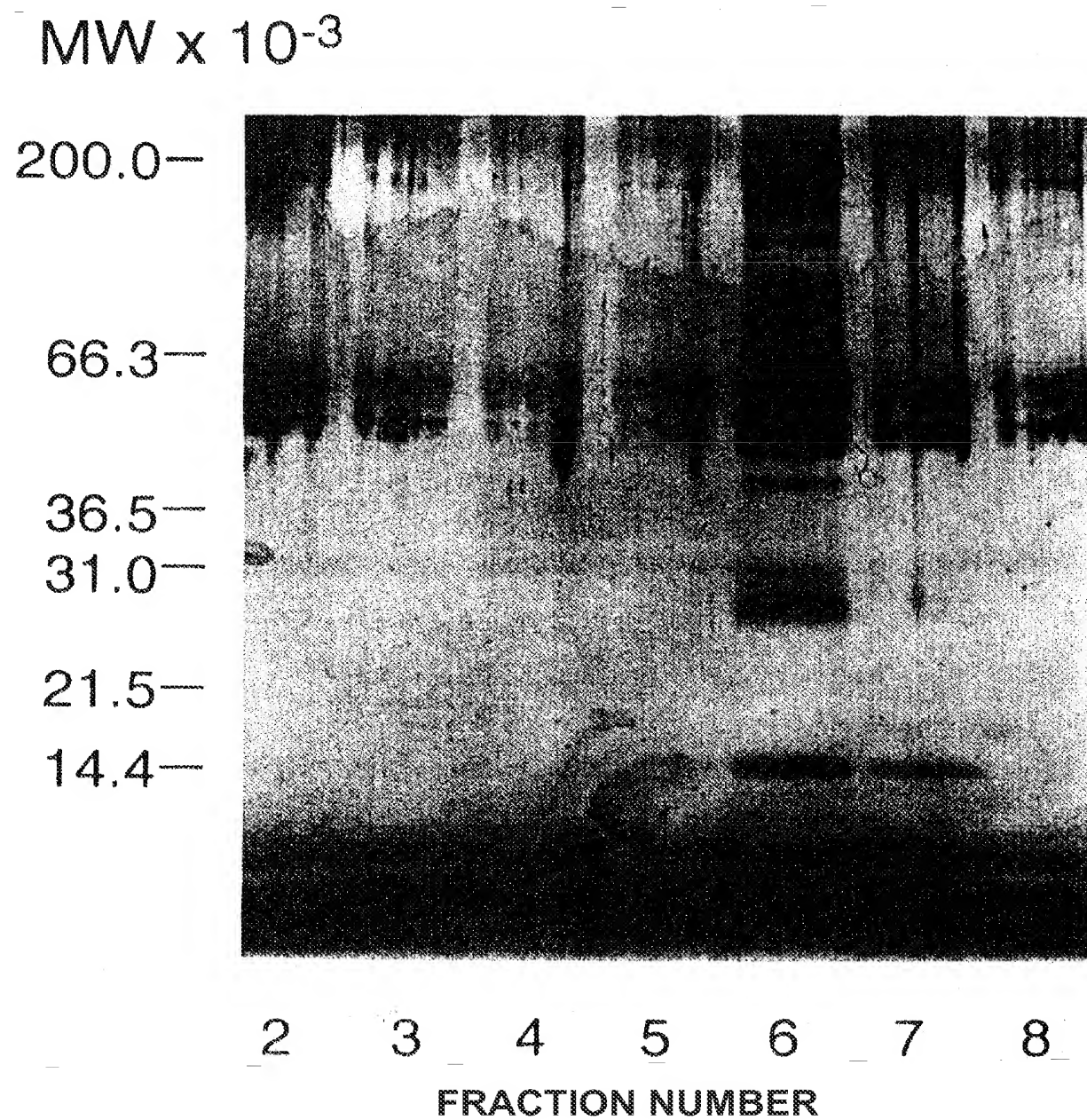


FIG. 4

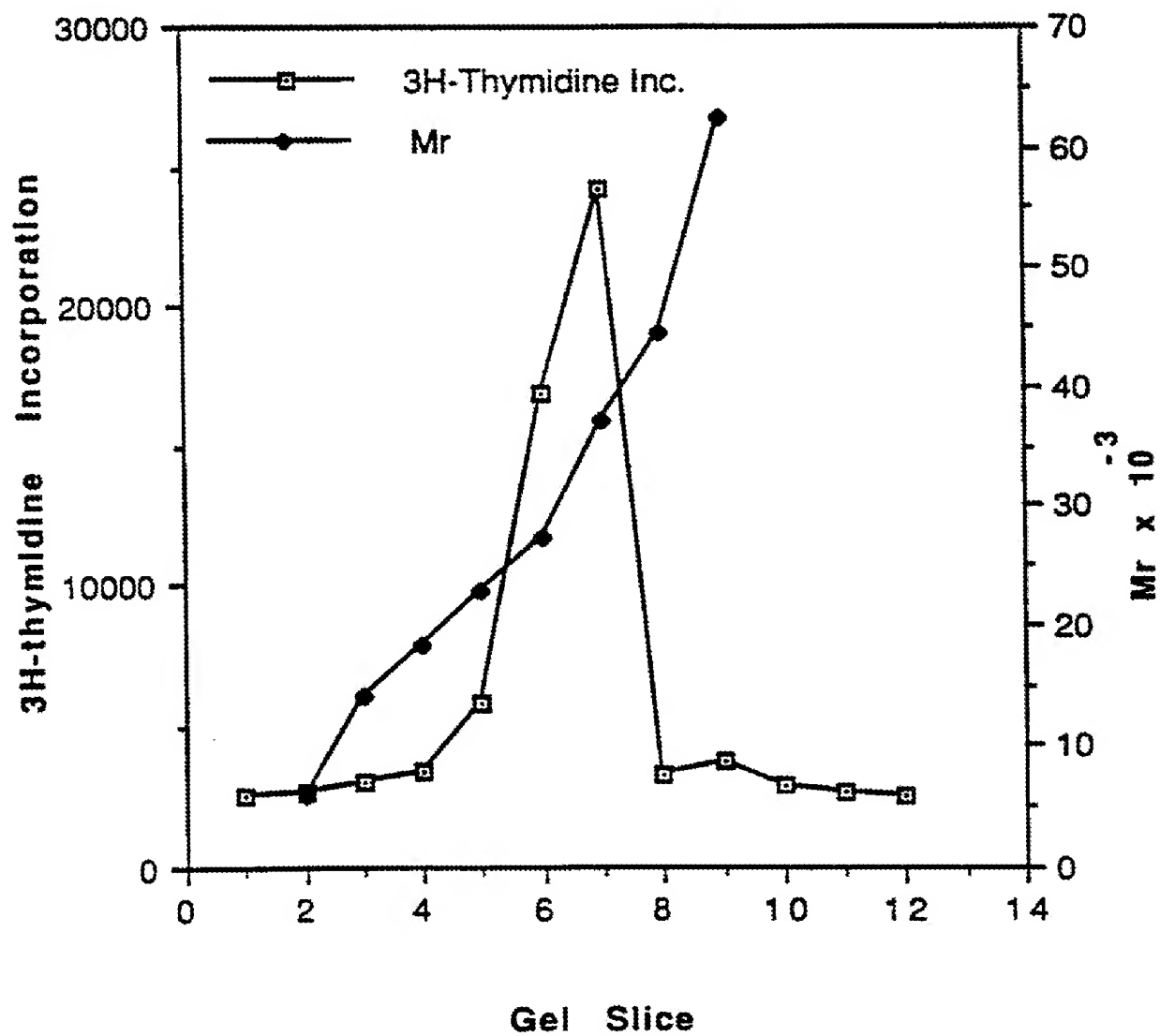


FIG. 5

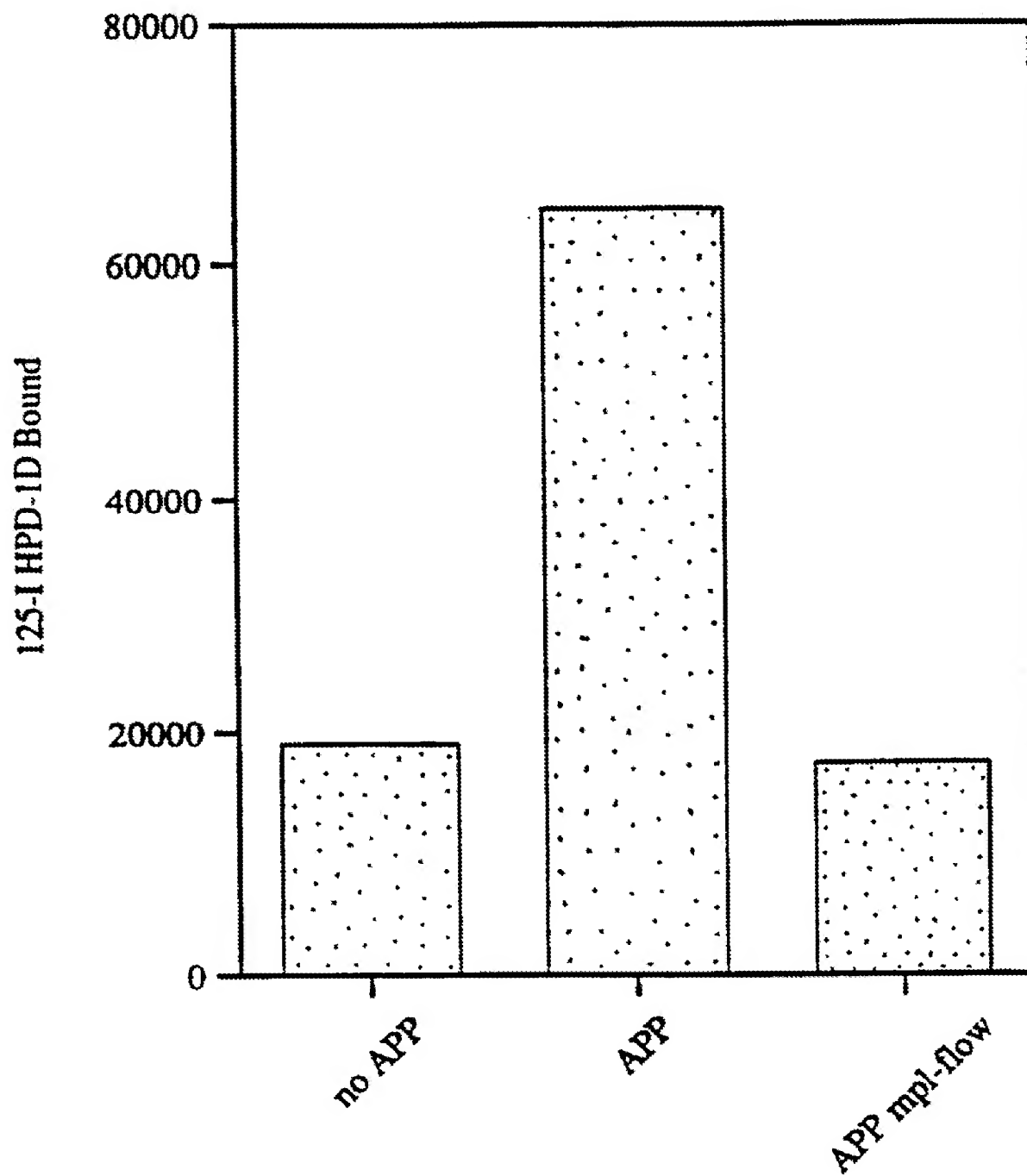


FIG. 6

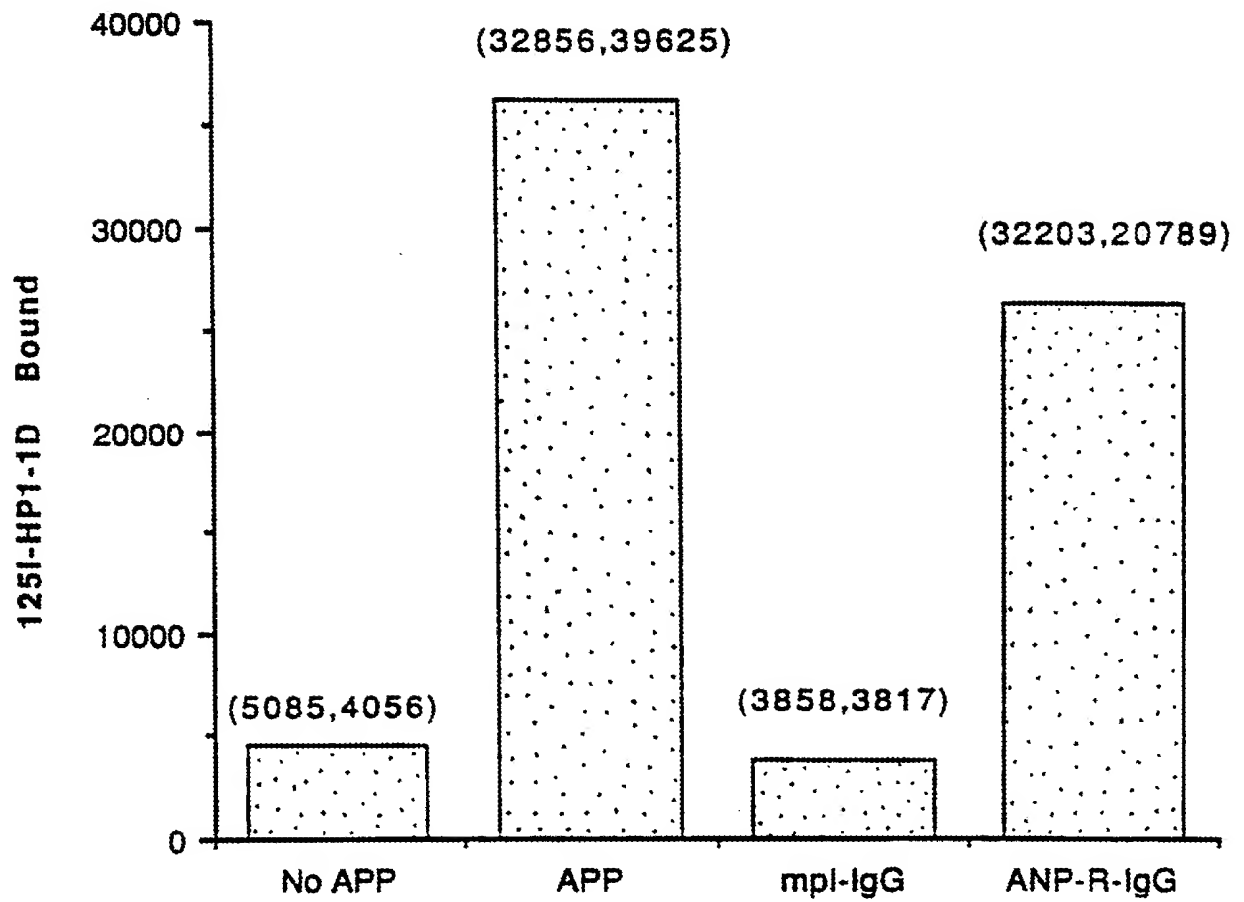


FIG. 7

1 GAATTCCTGG AATACCAGCT GACAATGATT TCCTCCTCAT CTTTCAACCT CACCTCTCCT CATCTAAGAA TTGCTCCTCG TGGTCATGCT TCTCCTAACT
CTTAAGGACC TTATGGTCGA CTGTTACTAA AGGAGGAGTA GAAAGTTGGA GTGGAGAGGA GTAGATTCTT AACGAGGAGC ACCAGTACGA AGAGGATTGA
↓ L L L V V M L L L T
-10

101 GCAAGGCTAA CGCTGTCCAG CCGGGCTCCT CCTGCTTGTG ACCTCCGAGT CCTCAGTAAA CTGCTTGTG ACTCCCATGT CCTTCACAGC AGACTGGTGA
CGTTCCGATT GCGACAGGTC GGGCCGAGGA GGACGAACAC TGGAGGCTCA GGAGTCATTT GACGAAGCAC TGAGGGTACA GGAAGTGTG TCTGACCACT
A R L T L S S P A P P A C D L R V L S K L L R D S H V L H S R L
20

201 GAACTCCCAA CATTATCCC TTTATCCGG TAACTGGTAA GACACCCATA CTCCCAGGAA GACACCATCA CTTCTCTTAA CTCCTTGACC CAATGACTAT
CTTGAGGGTT GTAATAGGGG AATAGGCGC ATTGACCAAT CTGTGGGTAT GAGGGTCCCT CTGTGGTAGT GAAGGAGATT GAGGAACCTGG GTTACTGATA

301 TCTTCCCAT TTTGTCCTCC CTAATGATCA CACTCTCTGA CAAGAATTAT TCTTCACAAT ACAGCCCGCA TTTTAAAAGCT CTCGTCTAGA
AGAAGGGTAT AACAGGGGTG GATGACTAGT GTGAGAGACT GTTCTTAATA AGAAGTGTTA TGTCGGGGCGT AAATTTTCGA GAGCAGATCT

1 GCGTCTTCCT ACCCATCTGC TCCACAGAGG GCTGCCCTGCT GTGCACTTGG GTCCCTGGAGC CCTTCTCCAC CCGGATAGAT TCCTCACCCCT TGGCCCGGCCT
 CGCAGAAGGA TGGGTAGACG AGGGTCTCC CGACGGACGA CACGTGAACC CAGGACCTCG CAGGACCTCG GGCCTATCTA AGGAGTGGG ACCGGGGCGGA
 101 TTGCCCCACC CTACTCTGCC CAGAACTGCA AGAGCCTAAG CCGCCTCCAT GGCCCCCAGGA AGGATTCAAG GGAGAGGCC CAAACAGGGA GCCACGCCAG
 AACGGGTGG GATGAGACGG GTCTTACGT TCTGGATTG GCGGGAGGTA CCGGGTCTCT CCGGAGTCC TCTTAAAGTCC CTTCTCCGGG GTTTGTCCCT CGGTGCGGTC
 Me tGluLeuThr GluLeuLeuL euValValMe tLeuLeuLeu ThrAlaArgL euThrLeuSe rSerProAla ProProAlaCys
 201 CCAGACACCC CGGCCAGAAAT GGAGCTGACT GAAATGCTCC TCGTGGTCAT GCTTCTCCTA ACTGCAAGGC TAACGCTGTC CAGCCCGGCT CCTCTGCTT
 GGTCGTGGG GCCGGTCTTA CCTGACTGA CTTAACGAGG AGCACCACTA CAAAGAGGAT TGACGTTCGG ATTGCGACAG GTCGGGCCGA GGAGGACGAA
 AspLeuAr qValLeuSer LysLeuLeuA rAspSerHi sValLeuHis SerArgLeuS erGlnCysPr oGluValHis ProLeuProT hrProValLeu
 301 GTGACCTCCG AGTCTCAGT AAACCTGCTC TGACTCCCA TGCTCTTCC AGCAGACTGA GCCAGTGCC AGAGGTTTAC CCTTGCCTA CACCTGTCTT
 CACTGGAGGC TCAGGAGTCA TTGACGAAG CACTGAGGT ACAGGAAGTG TCGTCTGACT CCGTCAAGG TCTCCAAGTG GAAACGGAT GTGGACAGGA
 LeuProAla ValAspPheS erLeuGlyG lTrpLysThr GlnMetGluG luThrLysAl aGlnAspIle LeuGlyAlaV aThrLeuLe uLeuGluGly
 401 GCTGCCCTGCT GTGGACTTGA GCTTGGGAGA ATGGAATAACC CAGATGGAGG AGACCAAGGC ACAGGACATT CTGGGAGCAG TGACCTTCTT GCTGGAGGGA
 CGACGGACGA CACCTGAAAT CGAACCTCTT TACCTTTTGG GTCTACCTCC TCTGGTTCGG TGTCTGTAA GACCTCTGTC ACTGGGAAGA CGACCTCTCT
 ValMetAlaA laArgGlyG l nLeuGlyPro ThrCysLeuS erSerLeuLe uGlyGlnLeu aArgLeuLe uLeuGlyAla LeuGlnSerLeu
 501 GTGATGGCAG CACGGGGACA ACTGGGACCC ACTTGCCTCT CATCCCTCTT GGGGCAGCTT TCTGGACAGG TCCGTCTCTT CCTTGGGGCC CTGCAGAGCC
 CACTACCGTC GTGCCCCCTGT TGACCCCTGGG TGAACGGAGA GTAGGGAGGA CCCCCCTGAA AGACCTGTCC AGGCAGAGGA GGAACCCCCG GACGTCTCTCG
 LeuGlyTh rGlnLeuPro ProGlnGlyA rgThrThrAl aHisLysAsp ProAsnAlaI lePheLeuSe rPheGlnHis LeuLeuArgG lyLysValArg
 601 TCCTTGGAAC CCAGCTTCTT CCACAGGGCA GGACCACAGC TCACAAGGAT CCCAATGCCA TCTTCTGAG CTTCCACAC CTGCTCCGAG GAAAGGTGG
 AGGAACCTTG GGTGCAAGGA GGTGTCCCGT CCTGGTCTG AGTGTCTTA GGGTTACGGT AGAAGGACTC GAAGGTGTG GACGAGGCTC CTTTCCACGC
 PheLeuMet LeuValGlyG lySerThrLe uCysValArg ArgAlaProP roThrThrAl aValProSer ArgThrSerL euValLeuTh rLeuAsnGlu
 701 TTTCCTGATG CTGTAGGAG GGTCACCCCT CTGCGTCAGG CCGGGCCCCAC CCACCACAGC TGTCCTGAG TGTCCTCTC TAGTCTCAC ACTGAACGAG
 AAAGGACTAC GAACATCCTC CCAGGTGGGA GACGCAGTCC GCCCGGGGTG GGTGGTGTG ACAGGGGTG TCTTGGAGAG ATCAGGAGTG TGACTTGCTC
 LeuProAsnA rgThrSerGl yLeuLeuGlu ThrAsnPheT hrAlaSerAl aArgThrThr GlySerGlyL euLeuLysTr pGlnGlnGly PheArgAlaLys
 801 CTCCCAACA GGACTTCTG ATTTTGGAG ACAAACTTCA CTGCTCAGC CAGAACTACT GGCCTTGGG TTTCTGAAGT GCAGCAGGGA TTCAGAGCCA
 GAGGTTTGT CCTGAAGACC TAACAACCTC TGTTTGAAGT GACGGAGTGG GTCTTGATGA GTCCTGATG CCGAGACCCG AAGACTTAC CGTCTCCCT AAGTCTCGT

Figure 8a

220	IleProGly	yLeuLeuAsn	GlnThrSerA	rgSerLeuAs	pGlnIlePro	GlyTyrLeuA	snArgIleHi	sGluLeuLeu	AsnGlyThrA	rgGlyLeuPhe	240
901	AGATTCTCTGG	TCTGCTGAAC	CAAACTCCA	GGTCCCTGGA	CCAAATCCCC	GGATACCTGA	ACAGGATACA	CGAACTCTTG	AATGGAACTC	GTGGACTCTT	
	TCTAAGGACC	AGACGACTTG	GTTTGAGGT	CCAGGGACCT	GGTTTAGGG	CCTATGGACT	TGTCCTATGT	GCTTGAGAAC	TTACCTTGAG	CACCTGAGAA	
250	ProGlyPro	SerArgArgT	hrLeuGlyAl	aProAspIle	SerSerGlyT	hrSerAspTh	rgGlySerLeu	ProProAsnL	euGlnProGly	yTyrSerPro	270
1001	TCCTGGACCC	TCACGCAGGA	CCCTAGGAGC	CCCGGACATT	TCCTCAGGAA	CATCAGACAC	AGGCTCCCTG	CCACCCAAACC	TCCAGCCTGG	ATATTCTCCT	
	AGGACCTGGG	AGTGCCTCT	GGGATCCTCG	GGGCCTGTAA	AGGAGTCCTT	GTAGTCTGTG	TCCGAGGGAC	GGTGGTTGG	AGGTCGGACC	TATAAGAGGA	
280	SerProThrH	isProProTh	rgGlyGlnTyr	ThrLeuPheP	roLeuProPr	oThrLeuPro	ThrProValV	alGlnLeuHi	sProLeuLeu	ProAspProSer	300
1101	TCCCCAACCC	ATCCTCCTAC	TGGACAGTAT	ACGCTCTTCC	CTCTTCCACC	CACCTTGCCC	ACCCCTGTGG	TCCAGCTCCA	CCCCCTGCTT	CCTGACCCCTT	
	AGGGGTTGGG	TAGGAGGATG	ACCTGTCATA	TGCAGAGGAG	GAGAAGGTGG	GTGGAACGGG	TGGGACACCC	AGGTCAGGT	GGGGGACGAA	GGACTGGGAA	
310	AlaProTh	rProThrPro	ThrSerProL	euLeuAsnTh	rSerTyrThr	HiSerGlnA	snLeuSerGly	nGluGly			320
1201	CTGCTCCAAC	GCCCACCCCT	ACCAGCCCTC	TTCTAAACAC	ATCCTACACC	CACCTCCAGA	ATCTGTCTCA	GGAAAGGTAA	GGTTCCTAGA	CACTGCCGAC	
	GACGAGGTTG	CGGGTGGGA	TGGTCGGGAG	AAGATTGTGG	TAGGATGTGG	GTGAGGGTCT	TAGACAGAGT	CCTTCCCAT	CCAAGAGTCT	GTGACGGCTG	
1301	ATCAGCATTG	TCTCATGTAC	AGCTCCCTTC	CCTGCAGGGC	GCCCCTGGGA	GACAACCTGGA	CAAGATTTC	TACTTCTCC	TGAAACCCAA	AGCCCTGGTA	
	TAGTCGTAAC	AGAGTACATG	TCGAGGGAAG	GGACGTCCCG	CGGGGACCCCT	CTGTTGACCT	GTTCTAAAGG	ATGAAAGAGG	ACTTTGGGTT	TCGGGACCAT	
1401	AAAGGGATAC	ACAGGACTGA	AAAGGGAATC	ATTTTTCAC	GTACATTATA	AACCTTCAGA	AGCTATTTT	TTAAGCTATC	AGCAATACTC	ATCAGAGCAG	
	TTTCCCTATG	TGTCCTGACT	TTTCCCTTAG	TAAAAAGTGA	CATGTAATAT	TTGGAAGTCT	TCGATAAAAA	AATTCGATAG	TCGTTATGAG	TAGTCTCGTC	
1501	CTAGCTCTTT	GGTCTATTTT	CTGCAGAAAT	TTGCAACTCA	CTGATTCTCT	ACAATGCTCT	TTTCTGTGAT	AACTCTGCAA	AGGCCTGGGC	TGGCCTGGCA	
	GATCGAGAAA	CCAGATAAAA	GACGCTTTTA	AACGTTGAGT	GACTAAGAGA	TGTACGAGAA	AAAGACACTA	TTGAGACGTT	TCCGGACCCG	ACCGGACCGT	
1601	GTTGAACAGA	GGGAGAGACT	AACCTTGAGT	CAGAAAACAG	AGAAAGGGTA	ATTTCCTTIG	CTTCAAAATC	AAGGCCTTCC	AACGCCCCCA	TCCCCTTTAC	
	CAACTTGCT	CCCTCTCTGA	TTGGAACCTCA	GTCTTTTGTG	TCCTTCCCAT	TAAAGGAAAC	GAAGTTTAAG	TTCCGGAAGG	TTGCGGGGGT	AGGGGAAATG	
1701	TATCATCTC	AGTGGGACTC	TGATCCCAT	TTCTTAACAG	ATCTTTACTC	TTGAGAAATG	AATAAGCTTT	CTCTCAGAAA	AAAAAATAAA	AAAAAATAAA	
	ATAGTAAGAG	TCACCCCTGAG	ACTAGGGTAT	AAGAAATTGTC	TAGAAATGAG	AACCTTTTAC	TTATTCGAAA	GAGAGTCTTT	TTTTTTTTTT	TTTTTTTTTT	

Figure 8b

hmp11	1	MELTE	L	L	V	V	M	L	L	T	A	R	L	T	L	S	S	P	A	P	A	C	D	L	R	V	L	S	K	L	L	R	D	S	H	V	L	H												
hepo	1	M	G	V	H	E	C	P	A	W	L	L	L	S	L	P	L	G	L	P	V	L	G	A	P	P	R	L	I	C	D	S	R	V	L	E	R	Y	L	L	E	A	K	E	A	E					
hmp11	45	S	R	L	S	Q	C	P	E	V	H	P	L	P	T	P	V	L	L	P	A	V	D	F	S	L	G	E	W	K	T	Q	M	E	E	T	K	A	Q	D	I	L	G	A	V	T	L	L	E	G	
hepo	51	N	I	T	T	G	C	A	E	H	C	S	L	N	E	N	I	T	V	P	D	T	K	V	N	F	Y	A	W	K	R	M	E	V	G	Q	Q	A	V	E	V	W	Q	G	L	A	L	L	S	E	A
hmp11	95	V	M	A	A	R	G	Q	L	G	P	T	C	L	S	. .	S	L	L	G	Q	L	S	G	Q	V	R	L	L	. .	L	G	A	L	Q	S	L	L	G	T	Q	. .	L	P	P	Q	Q				
hepo	101	V	L	R	G	Q	A	L	L	V	N	S	S	Q	P	W	E	P	L	Q	L	H	V	D	K	A	V	S	G	L	R	S	L	T	T	L	L	R	A	L	G	A	Q	K	E	A	I	S	P	P	
hmp11	138	R	T	T	A	H	K	D	P	N	A	I	F	L	S	F	Q	H	L	L	R	G	K	V	R	F	L	. .	M	L	V	G	G	S	T	L	C	V	R	R	A	P	P	T	T	A	V	P	S		
hepo	151	A	A	S	A	P	L	R	T	I	T	A	D	T	F	R	K	L	F	R	V	Y	S	N	F	L	R	G	K	L	K	L	Y	T	G	E	A	C	R	T	G	D	R								
hmp11	185	R	T	S	L	V	L	T	L	N	E	L	P	N	R	T	S	G	L	L	E	T	N	F	T	A	S	A	R	T	T	G	S	G	L	L	K	W	Q	Q	G	F	R	A	K	I	P	G	L	L	N
hmp11	235	Q	T	S	R	S	L	D	Q	I	P	G	Y	L	N	R	I	H	E	L	L	N	G	T	R	G	L	F	P	G	P	S	R	R	T	L	G	A	P	D	I	S	S	G	T	S	D	T	G	S	L
hmp11	285	P	P	N	L	Q	P	G	Y	S	P	S	P	T	H	P	P	T	G	Q	Y	T	L	F	P	L	P	P	T	L	P	T	P	V	V	Q	L	H	P	L	L	P	D	P	S	A	P	T	P	T	
hmp11	335	T	S	P	L	L	N	T	S	Y	T	H	S	Q	N	L	S	Q	E	G																															

Figure 9

